

SEQUENCE LISTING

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<120> Novel Single Nucleotide Polymorphisms for Olfactory
Receptor-like Polypeptides and Nucleic Acids Encoding
the Same

<130> 15966-654 CIP

<140> 09/974,591

<141> 2001-10-09

<150> 60/245,292

<151> 2000-11-02

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<170> PatentIn Ver. 2.1

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 Ala Leu Gln Met Phe Leu Ala Leu Thr Met Gly Gly Ala Glu Asp Leu
 110 115 120

cta ctg gcc ttc atg gcc tat gac agg tat gtg gcc att tgt cat cct 437
 Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro
 125 130 135

ctg aca tac atg acc ctc atg agc tca aga gcc tgc tgg ctc atg gtg 485
 Leu Thr Tyr Met Thr Leu Met Ser Ser Arg Ala Cys Trp Leu Met Val
 140 145 150

gcc acg tcc tgg atc ctg gca tcc cta agt gcc cta ata tat acc gtg 533
 Ala Thr Ser Trp Ile Leu Ala Ser Leu Ser Ala Leu Ile Tyr Thr Val
 155 160 165

tat acc atg cac tat ccc ttc tgc agg gcc cag gag atc agg cat ctt 581
 Tyr Thr Met His Tyr Pro Phe Cys Arg Ala Gln Glu Ile Arg His Leu
 170 175 180 185

ctc tgt gag atc cca cac ttg ctg aag ttg gcc tgt gct gat acc tcc 629
 Leu Cys Glu Ile Pro His Leu Leu Lys Leu Ala Cys Ala Asp Thr Ser
 190 195 200

aga tat gag ctc atg gta tat gtg atg ggt gtg acc ttc ctg att ccc 677
 Arg Tyr Glu Leu Met Val Tyr Val Met Gly Val Thr Phe Leu Ile Pro
 205 210 215

tct ctt gct gct ata ctg gcc tcc tat aga gaa att cta cta gct atc 721

12.3

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ctc cat atg cca tca aat gag ggg agg aag aaa gcc ctt gtc acc tgc 773
Leu His Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr Cys
235 240 245

tct tcc cac ctg act gtg gtt ggg atg ttc tat gga gct gcc aca ttc 821
Ser Ser His Leu Thr Val Val Gly Met Phe Tyr Gly Ala Ala Thr Phe
250 255 260 265

atg tat gtc ttg ccc agt tcc ttc cac agc acc aga caa gac aac atc 869
Met Tyr Val Leu Pro Ser Ser Phe His Ser Thr Arg Gln Asp Asn Ile
270 275 280

atc tct gtt ttc tac aca att gtc act cca gcc ctg aat cca ctc atc 917
Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu Ile
285 290 295

tac agc ctg agg aat aag gag gtc atg cgg gcc ttg agg agg gtc ctg 965
Tyr Ser Leu Arg Asn Lys Glu Val Met Arg Ala Leu Arg Arg Val Leu
300 305 310

gga aaa tac atg ctg cca gca cac tcc acg ctc tagggaagga 1008
Gly Lys Tyr Met Leu Pro Ala His Ser Thr Leu
315 320

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<210> 12
 <211> 324
 <212> PRT
 <213> Homo sapiens

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<400> 12
Met Glu Leu Trp Asn Tyr His Ser Met Glu Leu Trp Asn Phe Thr Leu
1 5 10 15

Gly Ser Gly Phe Ile Leu Val Gly Ile Leu Asn Asp Ser Gly Ser Pro
20 25 30

Glu Leu Leu Cys Ala Thr Ile Thr Ile Leu Tyr Leu Leu Ala Leu Ile
35 40 45

Ser Asn Gly Leu Leu Leu Leu Ala Ile Thr Met Glu Ala Arg Leu His
50 55 60

Met Pro Met Tyr Leu Leu Leu Gly Gln Leu Ser Leu Met Asp Leu Leu
65 70 75 80

Phe Thr Ser Val Val Thr Pro Lys Ala Leu Ala Asp Phe Leu Arg Arg
85 90 95

Glu Asn Thr Ile Ser Phe Gly Gly Cys Ala Leu Gln Met Phe Leu Ala
100 105 110

Leu Thr Met Gly Gly Ala Glu Asp Leu Leu Leu Ala Phe Met Ala Tyr
115 120 125

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130 135 140

Ser Ser Arg Ala Cys Trp Leu Met Val Ala Thr Ser Trp Ile Leu Ala
 145 150 155 160
 Ser Leu Ser Ala Leu Ile Tyr Thr Val Tyr Thr Met His Tyr Pro Phe
 165 170 175
 Cys Arg Ala Gln Glu Ile Arg His Leu Leu Cys Glu Ile Pro His Leu
 180 185 190
 Leu Lys Leu Ala Cys Ala Asp Thr Ser Arg Tyr Glu Leu Met Val Tyr
 195 200 205
 Val Met Gly Val Thr Phe Leu Ile Pro Ser Leu Ala Ala Ile Leu Ala
 210 215 220
 Ser Tyr Thr Gln Ile Leu Leu Thr Val Leu His Met Pro Ser Asn Glu
 225 230 235 240
 Gly Arg Lys Lys Ala Leu Val Thr Cys Ser Ser His Leu Thr Val Val
 245 250 255
 Gly Met Phe Tyr Gly Ala Ala Thr Phe Met Tyr Val Leu Pro Ser Ser
 260 265 270
 Phe His Ser Thr Arg Gln Asp Asn Ile Ile Ser Val Phe Tyr Thr Ile
 275 280 285
 Val Thr Pro Ala Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu
 290 295 300
 Val Met Arg Ala Leu Arg Arg Val Leu Gly Lys Tyr Met Leu Pro Ala
 305 310 315 320
 His Ser Thr Leu

<210> 13
 <211> 1008
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (27) .. (998)

<400> 13
 agctggagat ctggaacttc cacagc atg gag ctc tgg aac tac cac agc atg 53
 Met Glu Leu Trp Asn Tyr His Ser Met
 1 5

gaa ctc tag aac ttc acc tta gaa gat ggc ttc att tta gta gaa att 100

ctg aat gac agt ggg tct cct gaa ctg ctc tgt gct aca att aca atc 149
 Leu Asn Asp Ser Gly Ser Pro Glu Leu Leu Cys Ala Thr Ile Thr Ile
 30 35 40

cta tac ttg ttg gcc ctg atc agc aat ggc cta ctg ctc ctg gct atc 197
 Leu Tyr Leu Leu Ala Leu Ile Ser Asn Gly Leu Leu Leu Leu Ala Ile
 45 50 55

acc atg gaa gcc cgg ctc cac atg ccc atg tac ctc ctg ctt ggg cag 245
 Thr Met Glu Ala Arg Leu His Met Pro Met Tyr Leu Leu Leu Gly Gln
 60 65 70

ctc tct ctc atg gac ctc ctg ttc aca tct gtc gtc act ccc aag gcc 293
 Leu Ser Leu Met Asp Leu Leu Phe Thr Ser Val Val Thr Pro Lys Ala
 75 80 85

ctt gcg gac ttt ctg cgc aga gaa aac acc atc tcc ttt gga ggc tgt 341
 Leu Ala Asp Phe Leu Arg Arg Glu Asn Thr Ile Ser Phe Gly Gly Cys
 90 95 100 105

gcc ctt cag atg ttc ctg gca ctg aca atg ggt ggt gct gag gac ctc 389
 Ala Leu Gln Met Phe Leu Ala Leu Thr Met Gly Gly Ala Glu Asp Leu
 110 115 120

cta ctg gcc ttc atg gcc tat gac agg tat gtg gcc att tgt cat cct 437
 Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro
 125 130 135

ctg aca tac atg acc ctc atg agc tca aga gcc tgc tgg ctc atg gtg 485
 Leu Thr Tyr Met Thr Leu Met Ser Ser Arg Ala Cys Trp Leu Met Val
 140 145 150

gcc acg tcc tgg atc ctg gca tcc cta agt gcc cta ata tat acc gtg 533
 Ala Thr Ser Trp Ile Leu Ala Ser Leu Ser Ala Leu Ile Tyr Thr Val
 155 160 165

tat acc atg cac tat ccc ttc tgc agg gcc cag gag atc agg cat ctt 581
 Tyr Thr Met His Tyr Pro Phe Cys Arg Ala Gln Glu Ile Arg His Leu
 170 175 180 185

ctc tgt gag atc cca cac ttg ctg aag ttg gcc tgt gct gat acc tcc 629
 Leu Cys Glu Ile Pro His Leu Leu Lys Leu Ala Cys Ala Asp Thr Ser
 190 195 200

aga tat gag ctc atg gta tat gtg atg ggt gtg acc ttc ctg att ccc 677
 Arg Tyr Glu Leu Met Val Tyr Val Met Gly Val Thr Phe Leu Ile Pro
 205 210 215

tct ctt gct gct ata ctg gcc tcc tat aca caa att cta ctc act gtg 725
 Ser Leu Ala Ala Ile Leu Ala Ser Tyr Thr Gln Ile Leu Leu Thr Val
 220 225 230

ctc cat atg cca tca aat gag ggg agg aag aaa gcc ctt gtc acc tgc 773
 Leu His Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr Cys

Ser Ser His Leu Thr Val Val Gly Met Phe Tyr Gly Ala Ala Thr Phe
 250 255 260 265
 atg tat gtc ttg ccc agt tcc ttc cac agc acc aga caa gac aac atc 869
 Met Tyr Val Leu Pro Ser Ser Phe His Ser Thr Arg Gln Asp Asn Ile
 270 275 280
 atc tct gtt ttc tac aca att gtc act cca gcc ctg aat cca ctc atc 917
 Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu Ile
 285 290 295
 tac agc ctg agg aat aag gag gtc atg cgg gcc ttg agg agg gtc ctg 965
 Tyr Ser Leu Arg Asn Lys Glu Val Met Arg Ala Leu Arg Arg Val Leu
 300 305 310
 gga aaa tac atg ctg cca gca cac tcc acg ctc tagggaagga 1008
 Gly Lys Tyr Met Leu Pro Ala His Ser Thr Leu
 315 320

<210> 14
 <211> 324
 <212> PRT
 <213> Homo sapiens

<400> 14
 Met Glu Leu Trp Asn Tyr His Ser Met Glu Leu Trp Asn Phe Thr Leu
 1 5 10 15
 Gly Ser Gly Phe Ile Leu Val Gly Ile Leu Asn Asp Ser Gly Ser Pro
 20 25 30
 Glu Leu Leu Cys Ala Thr Ile Thr Ile Leu Tyr Leu Leu Ala Leu Ile
 35 40 45
 Ser Asn Gly Leu Leu Leu Leu Ala Ile Thr Met Glu Ala Arg Leu His
 50 55 60
 Met Pro Met Tyr Leu Leu Leu Gly Gln Leu Ser Leu Met Asp Leu Leu
 65 70 75 80
 Phe Thr Ser Val Val Thr Pro Lys Ala Leu Ala Asp Phe Leu Arg Arg
 85 90 95
 Glu Asn Thr Ile Ser Phe Gly Gly Cys Ala Leu Gln Met Phe Leu Ala
 100 105 110
 Leu Thr Met Gly Gly Ala Glu Asp Leu Leu Leu Ala Phe Met Ala Tyr
 115 120 125
 Asp Arg Tyr Val Ala Ile Cys His Pro Leu Thr Tyr Met Thr Leu Met
 130 135 140
 Ser Ser Arg Ala Cys Trp Leu Met Val Ala Thr Ser Thr Ile Tyr Ala
 145 150 155 160 165 170 175 180 185 190 195 200
 Met Leu Ser Ala Leu Thr Tyr Thr Val Tyr Thr Met His Tyr Pro Phe

<210> 16
 <211> 312
 <212> PRT
 <213> Mus musculus

<400> 16

Met Glu Pro Ser Asn Arg Thr Ala Val Ser Glu Phe Val Leu Lys Gly
 1 5 10 15

Phe Ser Gly Tyr Pro Ala Leu Glu Arg Leu Leu Phe Pro Leu Cys Ser
 20 25 30

Val Met Tyr Leu Val Thr Leu Leu Gly Asn Thr Ala Ile Val Ala Val
 35 40 45

Ser Met Leu Asp Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Gly
 50 55 60

Asn Leu Ser Ile Leu Asp Ile Cys Tyr Thr Ser Thr Phe Val Pro Leu
 65 70 75 80

Met Leu Val His Leu Leu Ser Ser Arg Lys Thr Ile Ser Phe Thr Gly
 85 90 95

Cys Ala Val Gln Met Cys Leu Ser Leu Ser Thr Gly Ser Thr Glu Cys
 100 105 110

Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Gln
 115 120 125

Pro Leu Arg Tyr Pro Val Leu Met Ser His Arg Leu Cys Leu Met Leu
 130 135 140

Ala Gly Ala Ser Trp Val Leu Cys Leu Phe Lys Ser Val Ala Glu Thr
 145 150 155 160

Val Ile Ala Met Arg Leu Pro Phe Cys Gly His His Val Ile Arg His
 165 170 175

Phe Thr Cys Glu Ile Leu Ala Val Leu Lys Leu Thr Cys Gly Asp Thr
 180 185 190

Ser Val Ser Asp Ala Phe Leu Leu Val Gly Ala Ile Leu Leu Leu Pro
 195 200 205

Ile Pro Leu Thr Leu Ile Cys Leu Ser Tyr Met Leu Ile Leu Ala Thr
 210 215 220

Ile Leu Arg Val Pro Ser Ala Thr Gly Arg Ser Lys Ala Phe Ser Thr
 225 230 235 240

Cys Ser Ala His Leu Ala Val Val Leu Leu Phe Tyr Ser Thr Ile Ile
 245 250 255

Val Leu Val Val Val Val Val Val Val Val Val Val Val Val Val Val
 260 265 270

Val Phe Thr Val Leu Tyr Ala Val Val Thr Pro Met Leu Asn Pro Ile
275 280 285

Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Ala Arg Lys Ala
290 295 300

Trp Gly Ser Arg Trp Ala Cys Arg
305 310

<210> 17

<211> 162

<212> PRT

<213> Macaca sylvanus

<400> 17

Pro Ala Ile Cys Gln Pro Leu Arg Tyr Arg Val Leu Met Asn His Arg
1 5 10 15

Leu Cys Val Leu Leu Val Gly Ala Ala Trp Val Leu Cys Leu Leu Lys
20 25 30

Ser Val Thr Glu Thr Val Ile Ala Met Arg Leu Pro Phe Cys Gly His
35 40 45

His Val Val Ser His Phe Thr Cys Glu Ile Leu Ala Val Leu Lys Leu
50 55 60

Thr Cys Gly Asn Thr Ser Val Ser Glu Val Phe Leu Leu Val Gly Ser
65 70 75 80

Ile Leu Leu Leu Pro Val Pro Leu Ala Phe Ile Cys Leu Ser Tyr Leu
85 90 95

Leu Ile Leu Ala Thr Ile Leu Arg Val Pro Ser Ala Ala Gly Cys Arg
100 105 110

Lys Ala Phe Ser Thr Cys Ser Ala His Leu Ala Val Val Leu Leu Phe
115 120 125

Tyr Ser Thr Ile Ile Phe Thr Tyr Met Lys Pro Lys Ser Lys Glu Ala
130 135 140

His Ile Ser Asp Glu Val Phe Thr Val Leu Tyr Ala Met Val Thr Pro
145 150 155 160

Met Leu

<210> 18

<211> 312

<212> PPT

Met	Glu	Pro	Ser	Asn	Arg	Thr	Ala	Val	Ser	Glu	Phe	Val	Leu	Lys	Gly	1	5	10	15
Phe	Ser	Gly	Tyr	Pro	Ala	Leu	Glu	Arg	Leu	Leu	Phe	Pro	Leu	Cys	Ser	20	25	30	
Val	Met	Tyr	Leu	Val	Thr	Leu	Leu	Gly	Asn	Thr	Ala	Ile	Val	Ala	Val	35	40	45	
Ser	Met	Leu	Asp	Ala	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Gly	50	55	60	
Asn	Leu	Ser	Ile	Leu	Asp	Ile	Cys	Tyr	Thr	Ser	Thr	Phe	Val	Pro	Leu	65	70	75	80
Met	Leu	Val	His	Leu	Leu	Ser	Ser	Arg	Lys	Thr	Ile	Ser	Phe	Thr	Gly	85	90	95	
Cys	Ala	Val	Gln	Met	Cys	Leu	Ser	Leu	Ser	Thr	Gly	Ser	Thr	Glu	Cys	100	105	110	
Leu	Leu	Leu	Ala	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Leu	Ala	Ile	Cys	Gln	115	120	125	
Pro	Leu	Arg	Tyr	Pro	Val	Leu	Met	Ser	His	Arg	Leu	Cys	Leu	Met	Leu	130	135	140	
Ala	Gly	Ala	Ser	Trp	Val	Leu	Cys	Leu	Phe	Lys	Ser	Val	Ala	Glu	Thr	145	150	155	160
Val	Ile	Ala	Met	Arg	Leu	Pro	Phe	Cys	Gly	His	His	Val	Ile	Arg	His	165	170	175	
Phe	Thr	Cys	Glu	Ile	Leu	Ala	Val	Leu	Lys	Leu	Thr	Cys	Gly	Asp	Thr	180	185	190	
Ser	Val	Ser	Asp	Ala	Phe	Leu	Leu	Val	Gly	Ala	Ile	Leu	Leu	Leu	Pro	195	200	205	
Ile	Pro	Leu	Thr	Leu	Ile	Cys	Leu	Ser	Tyr	Met	Leu	Ile	Leu	Ala	Thr	210	215	220	
Ile	Leu	Arg	Val	Pro	Ser	Ala	Thr	Gly	Arg	Ser	Lys	Ala	Phe	Ser	Thr	225	230	235	240
Cys	Ser	Ala	His	Leu	Ala	Val	Val	Leu	Leu	Phe	Tyr	Ser	Thr	Ile	Ile	245	250	255	
Phe	Met	Tyr	Met	Lys	Pro	Lys	Ser	Lys	Glu	Ala	Arg	Ile	Ser	Asp	Gln	260	265	270	
Val	Phe	Thr	Val	Leu	Tyr	Ala	Val	Val	Thr	Pro	Met	Leu	Asn	Pro	Ile	275	280	285	

Trp Gly Ser Arg Trp Ala Cys Arg
305 310

<210> 19
<211> 305
<212> PRT
<213> Rattus norvegicus

<400> 19
Leu Leu Leu Gly Leu Ser Gly Tyr Pro Lys Thr Glu Ile Leu Tyr Phe
1 5 10 15

Val Ile Val Leu Val Met Tyr Leu Val Ile His Thr Gly Asn Gly Val
20 25 30

Leu Ile Ile Ala Ser Ile Phe Asp Ser His Leu His Thr Pro Met Tyr
35 40 45

Phe Phe Leu Gly Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Ser
50 55 60

Ser Val Pro Ser Thr Leu Val Ser Leu Ile Ser Lys Lys Arg Asn Ile
65 70 75 80

Ser Phe Ser Gly Cys Thr Val Gln Met Phe Val Gly Phe Ala Met Gly
85 90 95

Ser Thr Glu Cys Leu Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val
100 105 110

Ala Ile Cys Asn Pro Leu Arg Tyr Ser Val Ile Met Ser Lys Glu Val
115 120 125

Tyr Val Ser Met Ala Ser Ala Ser Trp Phe Ser Gly Gly Ile Asn Ser
130 135 140

Val Val Gln Thr Ser Leu Ala Met Arg Leu Pro Phe Cys Gly Asn Asn
145 150 155 160

Val Ile Asn His Phe Thr Cys Glu Val Leu Ala Val Leu Lys Leu Ala
165 170 175

Cys Ala Asp Ile Ser Leu Asn Ile Val Thr Met Val Ile Ser Asn Met
180 185 190

Ala Phe Leu Val Leu Pro Leu Leu Leu Ile Phe Phe Ser Tyr Val Leu
195 200 205

Ile Leu Tyr Thr Ile Leu Arg Met Asn Ser Ala Ser Gly Arg Arg Lys
210 215 220

Ala Phe Ser Thr Cys Ser Ala His Leu Thr Val Val Val Ile Phe Tyr
225 230 235 240

245 250 255

Gly Lys Asp Lys Phe Gln Thr Ser Asp Lys Ile Ile Ser Leu Phe Tyr
 260 265 270

Gly Val Val Thr Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn
 275 280 285

Lys Asp Val Lys Ala Ala Val Lys Tyr Ile Leu Lys Gln Lys Tyr Ile
 290 295 300

Pro
 305

<210> 20

<211> 309

<212> PRT

<213> Homo sapiens

<400> 20

Met Gly Phe Val Leu Leu Arg Leu Ser Ala His Pro Glu Leu Glu Lys
 1 5 10 15

Thr Phe Phe Val Leu Ile Leu Leu Met Tyr Leu Val Ile Leu Leu Gly
 20 25 30

Asn Gly Val Leu Ile Leu Val Thr Ile Leu Asp Ser Arg Leu His Thr
 35 40 45

Pro Met Tyr Phe Phe Leu Gly Asn Leu Ser Phe Leu Asp Ile Cys Phe
 50 55 60

Thr Thr Ser Ser Val Pro Leu Val Leu Asp Ser Phe Leu Thr Pro Gln
 65 70 75 80

Glu Thr Ile Ser Phe Ser Ala Cys Ala Val Gln Met Ala Leu Ser Phe
 85 90 95

Ala Met Ala Gly Thr Glu Cys Leu Leu Leu Ser Met Met Ala Phe Asp
 100 105 110

Arg Tyr Val Ala Ile Cys Asn Pro Leu Arg Tyr Ser Val Ile Met Ser
 115 120 125

Lys Ala Ala Tyr Met Pro Met Ala Ala Ser Ser Trp Ala Ile Gly Gly
 130 135 140

Ala Ala Ser Val Val His Thr Ser Leu Ala Ile Gln Leu Pro Phe Cys
 145 150 155 160

Gly Asp Asn Val Ile Asn His Phe Thr Cys Glu Ile Leu Ala Val Leu
 165 170 175

Lys Leu Ala Cys Ala Asp Ile Ser Ile Asp Val Ile Gln Met Gln Tyr

Leu Asn Val Ile Phe Leu Gly Val Pro Val Leu Phe Ile Ser Phe Ser

195

200

205

Tyr Val Phe Ile Ile Thr Thr Ile Leu Arg Ile Pro Ser Ala Glu Gly
210 215 220

Arg Lys Lys Val Phe Ser Thr Cys Ser Ala His Leu Thr Val Val Ile
225 230 235 240

Val Phe Tyr Gly Thr Leu Phe Phe Met Tyr Gly Lys Pro Lys Ser Lys
245 250 255

Asp Ser Met Gly Ala Asp Lys Glu Asp Leu Ser Asp Lys Leu Ile Pro
260 265 270

Leu Phe Tyr Gly Val Val Thr Pro Met Leu Asn Pro Ile Ile Tyr Ser
275 280 285

Leu Arg Asn Lys Asp Val Lys Ala Ala Val Arg Arg Leu Leu Arg Pro
290 295 300

Lys Gly Phe Thr Gln
305

<210> 21

<211> 1031

<212> DNA

<213> Homo sapiens

<400> 21

tgatggcaga ggggatatca catggaaaaa gccaatgaga cctcccctgt gatgggggttc 60
gttctctctga ggctctctgc ccaccagag ctggaaaaga cattcttcgt gctcatcctg 120
ctgatgtacc tcgtgatect gctgggcaat ggggtcctca tcctgggtgac catccttgac 180
tcccgctgc acacgccccat gtactttctt ctagggaacc tctccttctt ggacatctgc 240
ttcactacct cctcagtcct actggtcctg gacagctttt tgactcccca ggaaaccatc 300
tcctttctcag cctgtgctgt gcagatggca ctctcctttg ccatggcagg aacagagtgc 360
ttgctcctga gcatgatggc atttgatcgc tatgtggcca tctgcaaccc ccttaggtac 420
tccgtgatca tgagcaaggc tgcctacatg cccatggctg ccagctcctg ggctattggt 480
ggtgctgctt ccgtgggtaca cacatccttg gcaattcagc tgcccttctg tggagacaat 540
gtcatcaacc acttcacctg tgagattctg gctgttctaa agttggcctg tgctgacatt 600
tccatcaatg tgatcagcat ggaggtgacg aatgtgatct tcctaggagt cccggttctg 660
ttcatctctt tctcctatgt cttcatcctc accaccatcc tgaggatccc ctcagctgag 720
gggaggaaaa aggtcttctc cacctgctct gccacctca ccgtgggtgat cgtcttctac 780
gggaccttat tcttcatgta tgggaagcct aagtctaagg actccatggg agcagacaaa 840
gaggatcttt cagacaaact catccccctt ttctatgggg tggtgacccc gatgctcaac 900
cccacatctt atagcctgag gaacaaggat gtgaaggctg ctgtgaggag actgctgaga 960
ccaaaaggct tcaactcagt atggtggaag ggtcctctgt gattgtcacc cacatggaag 1020
taaggaatca c 1031

<210> 22

<211> 227

<212> PRT

<213> Rattus norvegicus

Leu Asn Leu Ser Phe Leu Asp Thr Cys Tyr Thr Thr Ser Ser Val Pro

1	5	10	15
Leu Ile Leu Gly Ser Phe Leu Thr Pro Arg Lys Thr Ile Ser Phe Ser			
20	25	30	
Gly Cys Ala Val Gln Met Phe Leu Ser Phe Ala Met Gly Ala Thr Glu			
35	40	45	
Cys Val Leu Leu Ser Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys			
50	55	60	
Asn Pro Leu Arg Tyr Pro Val Val Met Ser Lys Ala Val Tyr Val Pro			
65	70	75	80
Met Ala Thr Gly Ser Trp Ala Ala Gly Ile Ala Ala Ser Leu Val Gln			
85	90	95	
Thr Ser Leu Ala Met Arg Leu Pro Phe Cys Gly Asp Asn Val Ile Asn			
100	105	110	
His Phe Thr Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp			
115	120	125	
Ile Ser Ile Asn Ile Ile Ser Met Gly Val Thr Asn Val Ile Phe Leu			
130	135	140	
Gly Val Pro Val Leu Phe Ile Ser Phe Ser Tyr Ile Phe Ile Leu Ser			
145	150	155	160
Thr Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser			
165	170	175	
Thr Cys Ser Ala His Leu Thr Val Val Ile Val Phe Tyr Gly Thr Ile			
180	185	190	
Leu Phe Met Tyr Gly Lys Pro Lys Ser Lys Asp Pro Leu Gly Ala Asp			
195	200	205	
Lys Gln Asp Pro Ala Asp Lys Leu Ile Ser Leu Phe Tyr Gly Val Leu			
210	215	220	
Thr Pro Met			
225			

<210> 23
 <211> 319
 <212> PRT
 <213> Mus musculus

<400> 23
 Met Asp Arg Ser Asn Glu Thr Ala Pro Leu Ser Gly Phe Ile Leu Leu
 1 5 10 15

Leu Met Met Tyr Leu Val Ile Leu Leu Gly Asn Gly Val Leu Ile Leu
 35 40 45
 Val Ser Ile Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Gly Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Ser Ser Val Pro
 65 70 75 80
 Leu Ile Leu Asp Ser Phe Leu Thr Pro Arg Lys Thr Ile Ser Phe Ser
 85 90 95
 Gly Cys Ala Val Gln Met Phe Leu Ser Phe Ala Met Gly Ala Thr Glu
 100 105 110
 Cys Val Leu Leu Ser Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 Asn Pro Leu Arg Tyr Pro Val Val Met Asn Lys Ala Ala Tyr Val Pro
 130 135 140
 Met Ala Ala Ser Ser Trp Ala Gly Gly Ile Thr Asn Ser Val Val Gln
 145 150 155 160
 Thr Ser Leu Ala Met Arg Leu Pro Phe Cys Gly Asp Asn Val Ile Asn
 165 170 175
 His Phe Thr Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp
 180 185 190
 Ile Ser Ile Asn Val Ile Ser Met Val Val Ala Asn Met Ile Phe Leu
 195 200 205
 Ala Val Pro Val Leu Phe Ile Phe Val Ser Tyr Val Phe Ile Leu Val
 210 215 220
 Thr Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Ser Ala His Leu Thr Val Val Leu Val Phe Tyr Gly Thr Ile
 245 250 255
 Leu Phe Met Tyr Gly Lys Pro Lys Ser Lys Asp Pro Leu Gly Ala Asp
 260 265 270
 Lys Gln Asp Leu Ala Asp Lys Leu Ile Ser Leu Phe Tyr Gly Val Val
 275 280 285
 Thr Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val
 290 295 300
 Arg Ala Ala Val Arg Asn Leu Val Gly Gln Lys His Leu Thr Glu
 305 310 315

<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag431 PCR
Probe Sequence

<400> 24
agtcacttca cctgcaagat cct

23

<210> 25
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag431 PCR
Probe Sequence

<400> 25
ccgcatgccg gcttcagcac tg

22

<210> 26
<211> 19
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag431 PCR
Probe Sequence

<400> 26
cttcgctgac cgacgtggt

19